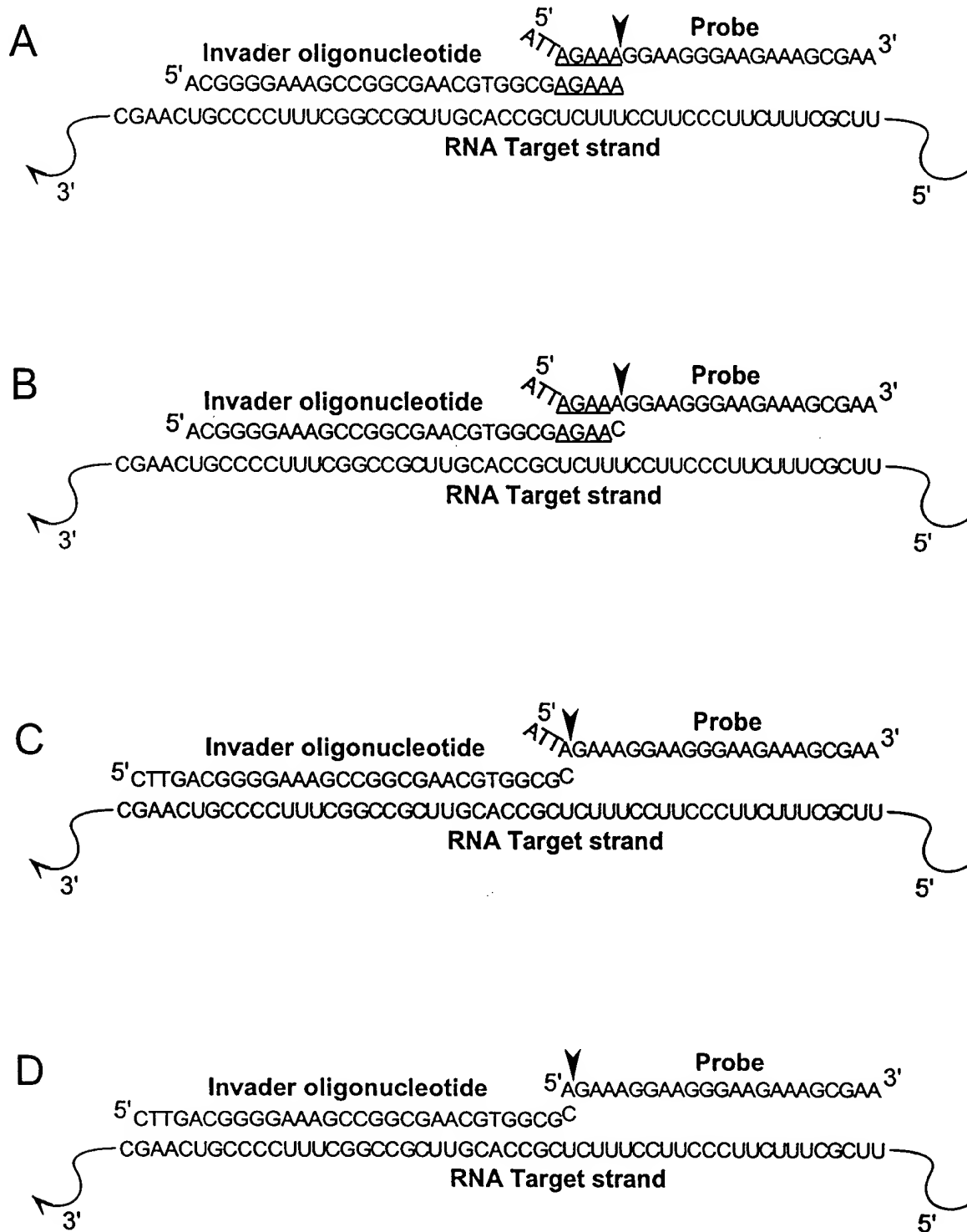
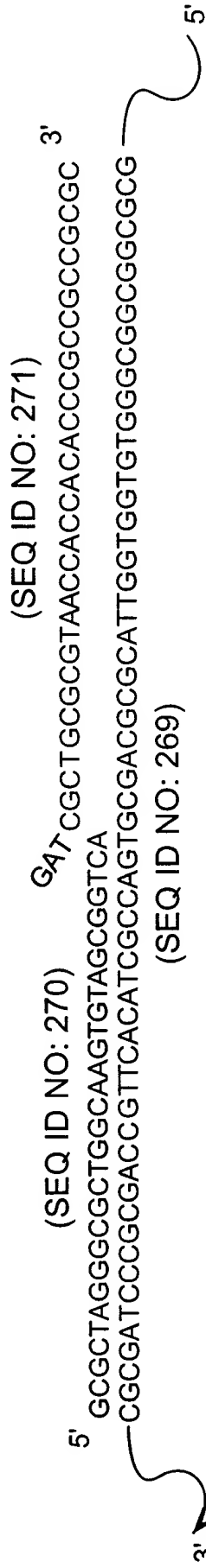


FIGURE 1

FIGURE 2



A



B

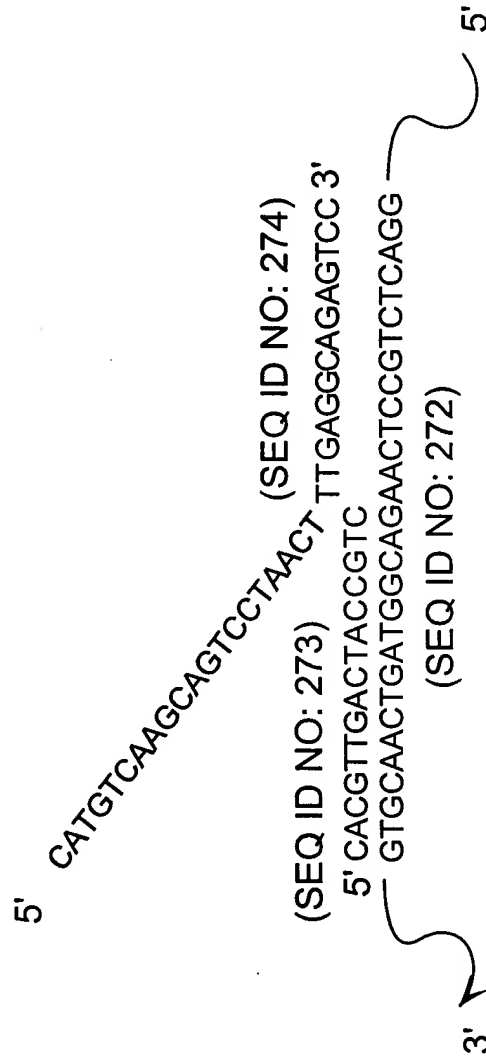


FIGURE 3

004390-002250

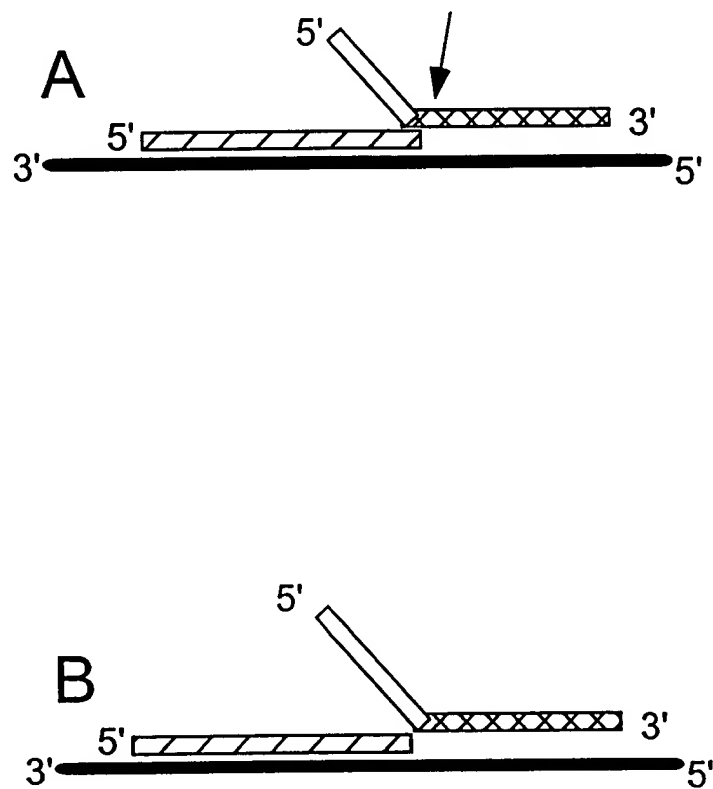


FIGURE 4

09577304 052400

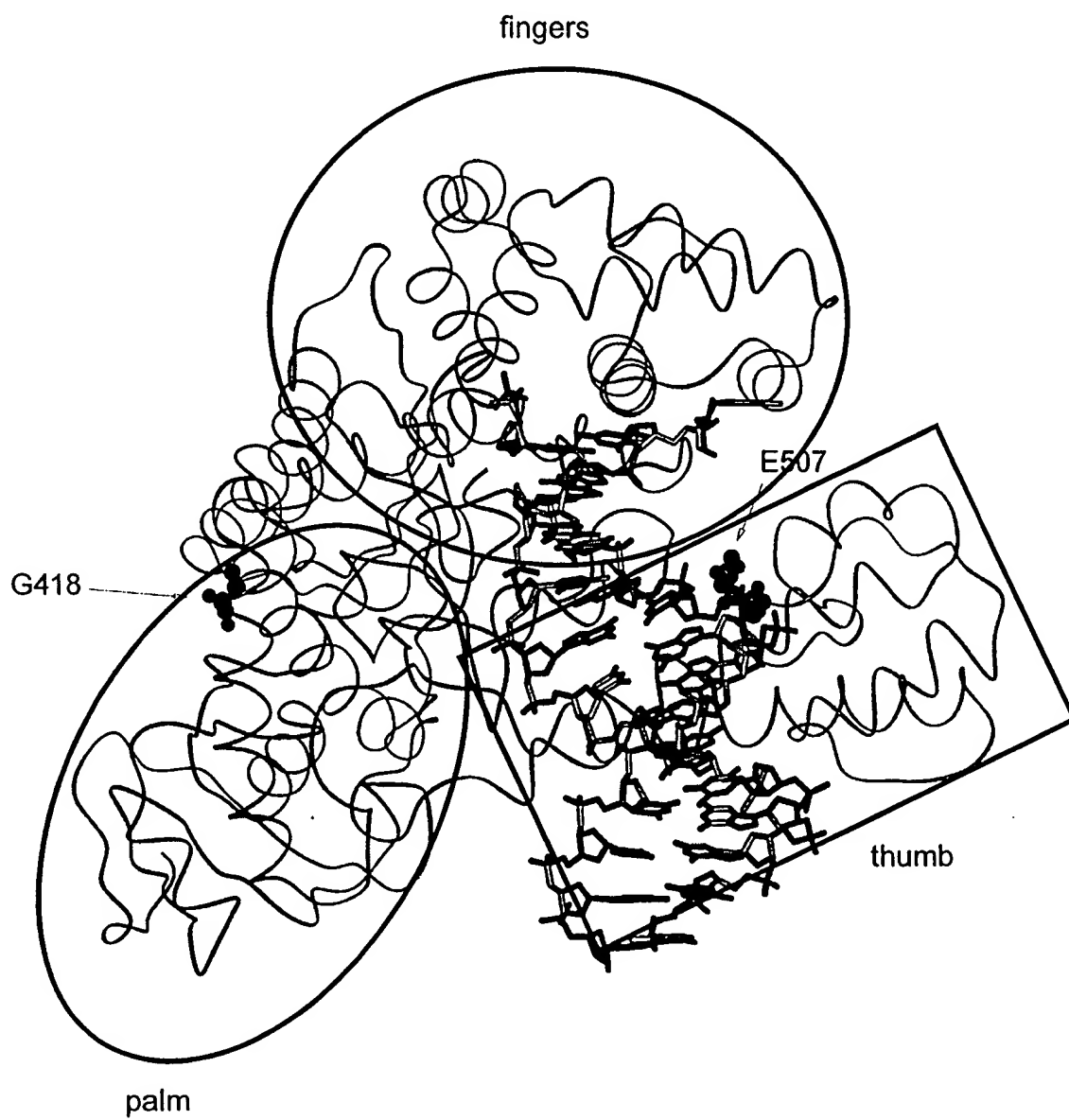


FIGURE 5

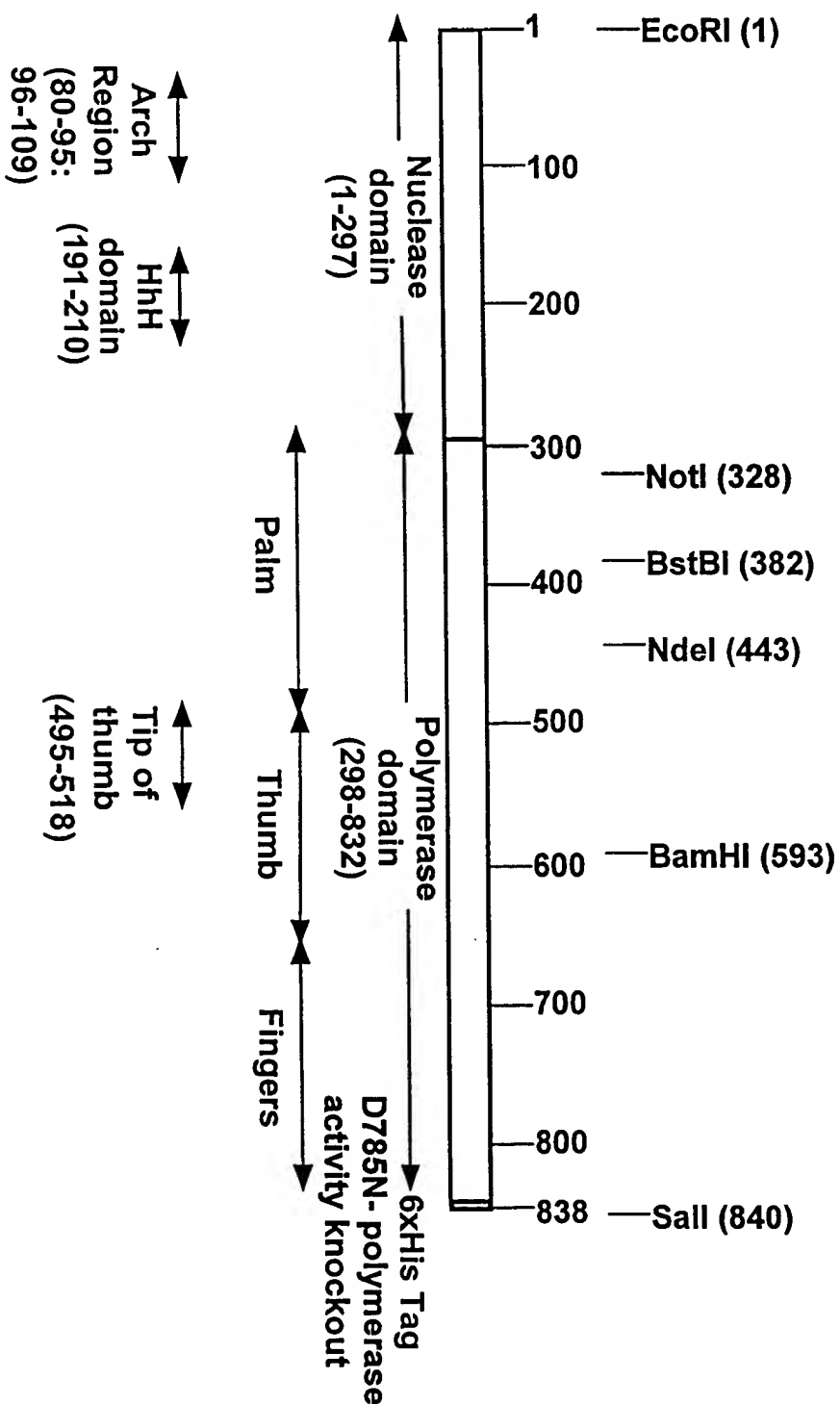


FIGURE 6

DNAPTAQA.....G.....G.....	347
DNAPTFLG.....T.....G.....	344
DNAPTHHT.....A.....	350

MAJORITY [SEQ ID NO:7] CGAGGGGAGGAGGTCTGGCCAGCCCTGGCCCAAGAGGGGAAAGGAGGGGTACGAGGTGGGCATCGCTC

DNAPTAO [SEQ ID NO:1]G.....G.....C.....G..... 417
DNAPTFL [SEQ ID NO:2] T.....G.....CG..... 414
DNAPTTH [SEQ ID NO:266] T..C..... 420

MAJORITY ACCGGGAGGGGAGCCTCTACGAGCTCCTTCGGACCGCATGGCCGTCCTCCACCCGAGGGGTACCTCA

DNAPTAOAAA.....T.....GA..... 487
DNAPTFL ..T.....G.....A.....T.....G. 484
DNAPTTHA..G.C.....G.....CC..... 490

MAJORITY TCACCGGGCGTGGCTTTGGAGAAAGTAGGGCTGAGGGCGGAGGAGTGGGTGGACTACGGGGCGCTGGC

DNAPTAOC.....A.....C.....C.....CC.....A. 557
DNAPTFLAC.....C.C..... 554
DNAPTTHA.....C.....T...C.....C.T 560

MAJORITY GGGGAGCCGCTCGGACAACCTCCCGGGGTCAGGGGCATCGGGGAGAAAGCGGGCCXGAAGCTCCTCXAG

DNAPTAO C.....GAG.....T.....G..GAG.....T..GG.. 627
DNAPTFLG..T..A.....G.....A..G....A..CGC 624
DNAPTTHT.....TC.....A.. 630

MAJORITY GAGTGGGGAGGCTGGAAAAAGCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC---CXTCCGGGAGAGAAGA

DNAPTAOGC.....C.....A..... 694
DNAPTFLT..C..G.....A.....T...T.G.....C 691
DNAPTTHA.....A.....A.AAAA.G..... 700

MAJORITY [SEQ ID NO:7] TCGAGGGCCACATGGAXGAGCTGAXGCTCTCGTGGGAGGCTXTCGAGAGGTGGCGACGGAGCCTGGCGGCTGGA

DNAPTAO [SEQ ID NO:1] ...T...C..T...A...C..GG..A... 764
DNAPTFL [SEQ ID NO:2] ...GGG...G.C...GCC.T...C.A...T...A...T... 761
DNAPTTH [SEQ ID NO:266]...A...C...A...C.G...T...C...G...C... 770

MAJORITY GGTGGACTTCGCCAAGXGGGGGAGCGCCGACCGGGAGGGGCTTAGGGCCCTTCTGGAGAGGCTGGAGCTT

DNAPTAOAA.....A.....T.....T..... 834
DNAPTFLGG.G.C.C..CACA...A...T.....T..GC...T...T...C..T... 831
DNAPTTHC.....C..G.....T.....C.....C.....C 840

MAJORITY GCGAGGCTCCTCCAGGAGTTCGGGCTCCTGGAGGGGGCCCAAGGCCCTGGAGGAGGGCCCTGGCGGCGGCGG

DNAPTAOT....AA..... 904
DNAPTFLA.....G..G....GGCA.....T. 901
DNAPTTHC.....C....GCCC..... 910

MAJORITY CGGAAGGGGCGCTTCGTGGGCTTGTCCCTTTCGGGCGCGGAGCGCATGTGGGCGGAGCTTCTGGCGGCTGGG

DNAPTAOT.....G.....AAG.....T..... 974
DNAPTFLT..TT.....TC.T.....T..... 971
DNAPTTHC.....C.....G.....AAA..... 980

MAJORITY CCGCGCCAGGGAGGGCGGCTCCACCGGGGACGAGCGCCCTTTAXGGGCGCTXAGGGAGCTXAAGGAGGTG

DNAPTAOG.....C..C..G..T.A..AA..C...G.....G.....C. 1044
DNAPTFL T.GG..GT.....G..CC...T.....A.....G...G...T...G... 1041
DNAPTTH ...TG.....C.....G.....GCG...G..A..A.....C.....C 1050

MAJORITY [SEQ ID NO:7] CCGGGXCTGCTGGCCAAAGGACCTGGCCGTTTGGCCCTGAGGGAGGGGCTXGACCTCXTGGCCGGGGAGG

DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T..G.....CC.....C..... 1114
 DNAPTFL [SEQ ID NO:2]AA.....G.....G.....C.....G.....T..C..A..A..... 1111
 DNAPTTH [SEQ ID NO:266]C.....C.....TC.....G..A.....G..... 1120

MAJORITY ACCCGATGCTGCTGGCTAGCTGCTGGACCGCTCCAACACACCCCGAGGGGCTGGCCGGGGCTACGG

DNAPTAQT..... 1184
 DNAPTFLG.....T.....T.....T..... 1181
 DNAPTTHT.....T.....G..... 1190

MAJORITY GCGGGAGTGGACGGAGGAGXCGGGGGAGGGGGCGCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXGGGAG

DNAPTAQG.....G.....GC...T.....GC...GCG.....GTG..G. 1254
 DNAPTFLT.....A.....GG.....C.C.....A..C.....AAA.... 1251
 DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

MAJORITY CCGCTTGAGGGGAGGAGGGCTCCTTTGGCTTTACGAGGAGGTGGAGAACCCCTTCCGGGGTCCCTGG

DNAPTAQA.G.....G.....G.....G.....GCT..... 1324
 DNAPTFLA...A..A..AC.C..G.....G.....G.....GT... 1321
 DNAPTTHC.....A.....C.....C.....A.....C..... 1330

MAJORITY CCCACATGGAGGGCCAGGGGGTXXCGGGCTGGACGTGGGCTAGCTCCAGGGGCTTCCCTGGAGGTGGCGGA

DNAPTAQGG.....G..C.....T...AG...T..G.....C.. 1394
 DNAPTFLC.....C.....G.....A.....A..C 1391
 DNAPTTHC.....A.....T.....T.....C.T..... 1400

FIGURE 8E

MAJORITY [SEQ ID NO:7] GGAGATCGGGCGGCTGGAGGAGGAGGTCTTCGGCCCTGGCGGGGACGCCCTTCAAGCTCAAGTCCCGGGGAG

DNAPTAO [SEQ ID NO:1]GC.....CC..... 1464
 DNAPTFL [SEQ ID NO:2]G.G....AG.G..... 1461
 DNAPTTH [SEQ ID NO:266]T.....G..... 1470

MAJORITY CAGCTGGAAAGGGTGCTCTTTCAGGAGCTXGGGCTTCGGGCCCATCGGCAAGACGGAGAGACXGGCAAGC

DNAPTAOC.....A..... 1534
 DNAPTFLGC.....G.G..G..T.....G..G..A.. 1531
 DNAPTTHTA.....T.G..G.....C.A.....A..... 1540

MAJORITY GGTCCAGCAGCGCGCGGTGCTGGAGCGCCCTXCGXGAGCGCCACGCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAOC.....C..C..... 1604
 DNAPTFLT.....G.A.....CGC..... 1601
 DNAPTTHG.....A.G.....C...C.. 1610

MAJORITY CCGGGAGGCTCAGCAAGCTCAAGAACAGCTAGATXGACCGCCTGGCGXGCGCTCGTCCAGCCGACGCGGGC

DNAPTAOG...G.....T.....G.A...A..... 1674
 DNAPTFLA.....G.C...G...A...G... 1671
 DNAPTTHG.G.....C.AAG.....G..... 1680

MAJORITY GCGCTCCAGACCGGCTTCAACGAGACGGCCACGGCGAGGCTTAGTAGCTCGGACCGCAAGCTGC

DNAPTAOG.....A.....T.....C.. 1744
 DNAPTFLC.....TCC..... 1741
 DNAPTTHG.....G..... 1750

MAJORITY [SEQ ID NO:7] AGAAGATCCCGCTCCGGACCCXCTGGGCCAGAGGATCCGCCGGGCCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAO [SEQ ID NO:1]G..T..G.....A..C.....G...C. 1814
 DNAPTFL [SEQ ID NO:2]G.....T.....G..C.....A.....C.....C..... 1811
 DNAPTTH [SEQ ID NO:266]CT.....T.....C.....T.....C.....T.....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTGGGCCACCTCTCCGGGGAGGAGAACCTG

DNAPTAO A.....T.....T.....A.....G.....C..... 1884
 DNAPTFLT..T.....G.....T.....T.....C..... 1881
 DNAPTTHT.....T.....G.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCAGGAGGGAGGAGATCCACAGCCAGAGCCGCCAGCTGGATGTTGGGGCTCCGCCCGGG

DNAPTAOC.....GG.....G... 1954
 DNAPTFLT.....A.....TT...C. 1951
 DNAPTTHA.....A..... 1960

MAJORITY AGCGCGTGGAGCCCTGATGCCCGGGGGCCAGAGCCATCAACTTCGGGGTCTCTACGGGCATGTCCCG

DNAPTAOA..G..A.....T.....G... 2024
 DNAPTFLA.....T.....G..... 2021
 DNAPTTHA.....GG..G.....C..... 2030

MAJORITY CCACCGCCTCTCCGAGGAGCTTGGCATCCGCTACGAGGAGCGGCTGGCCCTTCAATTGAGCGCTACTTCCAG

DNAPTAOA.....T.....CCA.....T... 2094
 DNAPTFLGG.....T..... 2091
 DNAPTTHTA..G.....T.....A.....A 2100

MAJORITY [SEQ ID NO:7] AGCTTCGCCCAAGGTGGGGGCGCTGGATTGAGAAGACCGCTGGAGGAGGGCAGGAGGGGGGTACGTGGAGA

DNAPTAQ [SEQ ID NO:1]

DNAPTFL [SEQ ID NO:2]

DNAPTTH [SEQ ID NO:266]

2164
2161
2170

MAJORITY CCGTCITCGGGCGGGGGGCTACGTGCCCCGACCGCTCAACGCCCGGGGTGAAGAGCGGTGCGGGGAGGGCGGGG

DNAPTAQ

DNAPTFL

DNAPTTH

2234
2231
2240

MAJORITY GGGCATGGCGCTTCAACATGCCCGTCCAGGGCACCGCGCGGACCGTCATGAAGCTGGCCATGGTGAAGCTC

DNAPTAQ

DNAPTFL

DNAPTTH

2304
2301
2310

MAJORITY TTGGCGGGGCTXCAGGAAATGGGGCGCAGGATGCTCCTXCAGGTCCACGACGAGCTGCTCGAGGGCGC

DNAPTAQ

DNAPTFL

DNAPTTH

2374
2371
2380

MAJORITY CCAAAGAGGGGGGAGGXGGTGGCGGCTTGGGCAAGGAGGTGATGGAGGGGGTCTATCCCGCTGGCCGT

DNAPTAQ

DNAPTFL

DNAPTTH

2444
2441
2450

MAJORITY [SEQ ID NO:7] GCGCGCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCGGGCCAAGGAGTAG

DNAPTAA	[SEQ ID NO:1]A.....GA	2499
DNAPTFL	[SEQ ID NO:2]CC.....	2496
DNAPTTH	[SEQ ID NO:266]T.....GT...	2505

TAQ PRO	S.	K.	D.	G.	PE. YKA.	A 348
TFL PRO	G. A.	L. SF.		G. WE. L.	O. R.	G. 347
TTH PRO	A. AP.			K.	C. D.	A. A. K. 350

MAJORITY [SEO ID NO:8] RGLLAKDLAVLALREGLDLXPGDDPML LAYLLDPSNTTPEGVARRYGGEWTE DAGERALLSERLFXNLXX

TAQ PRO	[SEO ID NO:4]	S	G. P	E	A	A	WG	418
TFL PRO	[SEO ID NO:5]	I	F. E		A	QT. KE	417	
TTH PRO	[SEO ID NO:267]	S	V	AH	HR	LK	420	

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRELEEEVFRLAGHPFNLNSRD

TAQ PRO	R	R	A	R	A	A	488
TFL PRO	K	E	R	EA. V. Q			487
TTH PRO	K	H		L			490

MAJORITY OLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG

TAQ PRO					S	D. I	558
TFL PRO				DR		A	557
TTH PRO	R	L	Q	H	V	S	560

MAJORITY RLHTRFNOTATATGRLSDDPNLQNI PVRTPLGORIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL

TAQ PRO				I	L		628
TFL PRO				V	V		627
TTH PRO				A	A		630

MAJORITY IRVFQEGRDIHTQTASWMFGVPPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAI PYEEAVAFIERYFQ

TAQ PRO	E	R			Q		698
TFL PRO		S	G		G	S	697
TTH PRO	K		V				700

FIGURE 9C

MAJORITY [SEQ ID NO:8] SFPKVRWIEKTL EGRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPVOGTAADLMK LAMVKL

TAO PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]	Y.....G.....R.	767
TTH PRO	[SEQ ID NO:267]K.....	770

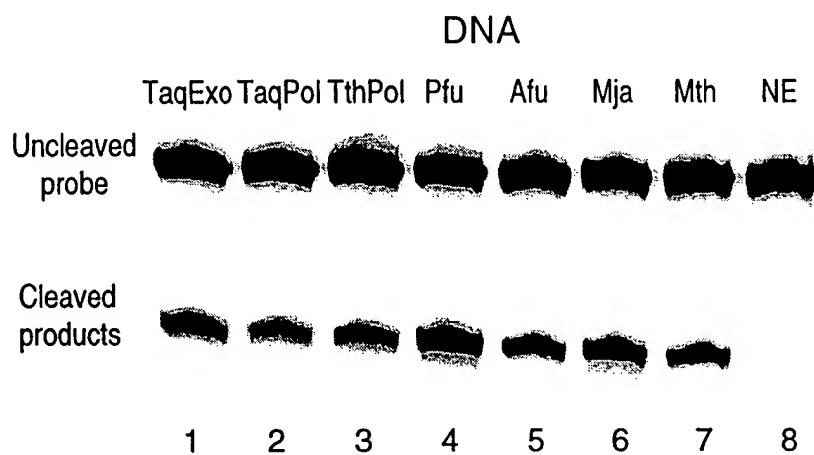
MAJORITY FPRLXEMGARM LQVHDELVL EAPKXRAEXVAA LAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAO PROE.....E...A...R.....I.....	833
TFL PROQ.L.....D...R.....W..O.....L.....	831
TTH PROR.....L....QA...E....A..KA.....M.....G	835

5'-F1-CGAAATTAAATTA
 Cleavage site
 Upstream probe
 5'-AGGAGAAGGCACTGGACCGAAGGC
 3'-...GGUCCCUUCCGUUGACCUUGCCGGAACAACCUUCCUCAAGUACGACCCGAG...-5'
 IL-6 RNA target strand
 3'-GGGTCCCTCTTCGGTTGACCTGGCTTCCGCGAACAACCTCTTCTCAAGTATCG-5'
 IL-6 DNA target strand

FIGURE 10

A



B

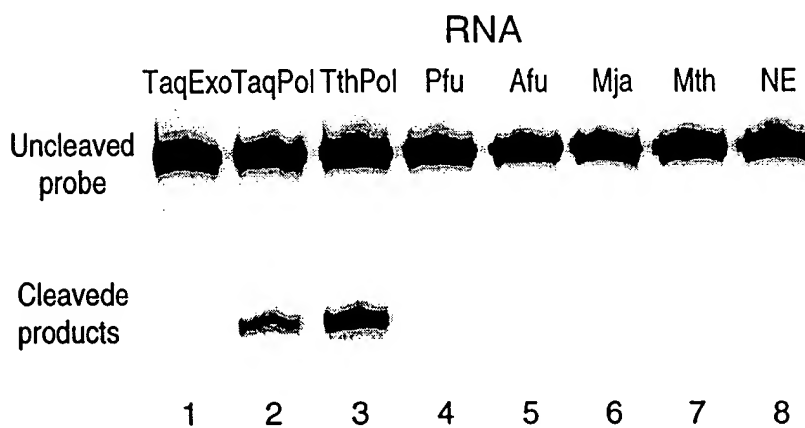


FIGURE 11

Enzyme Combination	Cycling Rate (min ⁻¹)
TaqPol	~0.3
TthPol	~0.85
TaqTth(N)	~0.85
TthTaq(N)	~0.35
TaqTth(B-S)	~0.55
TaqTth(N-B)	~1.4
TaqTth(N-D)	~0.35
TaqTth(D-B)	~0.4
TaqTth(Bs-B)	~0.85

FIGURE 12

[illegible]

FIGURE 13

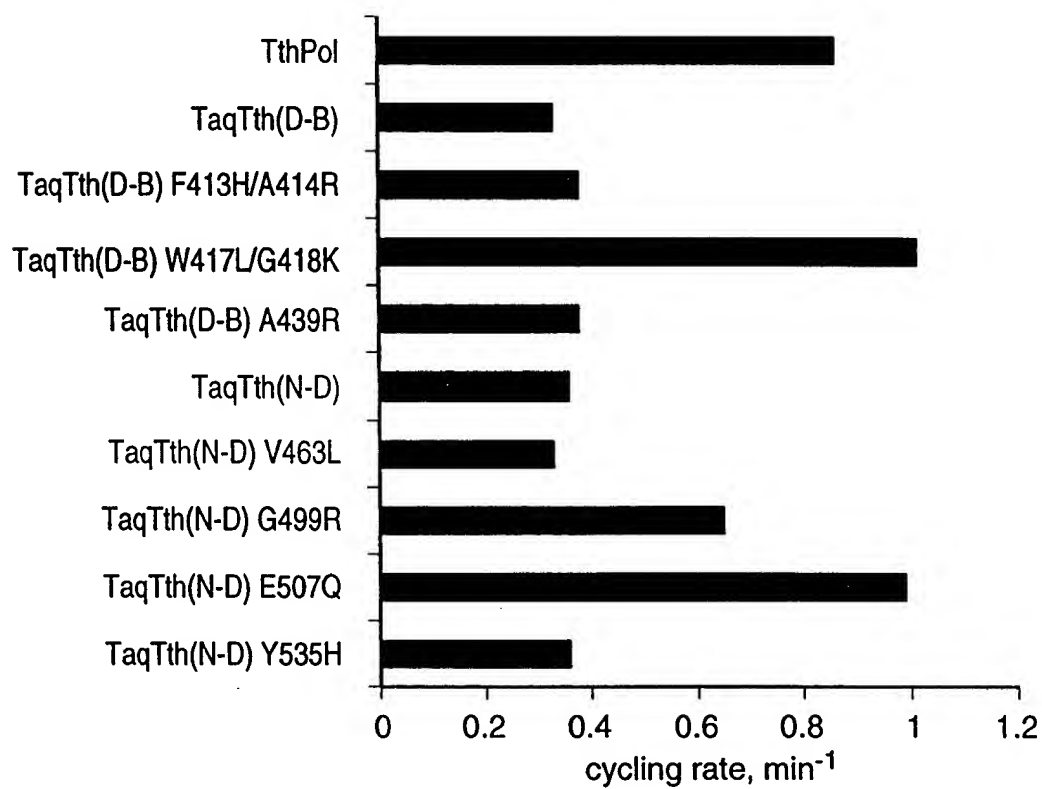


FIGURE 14

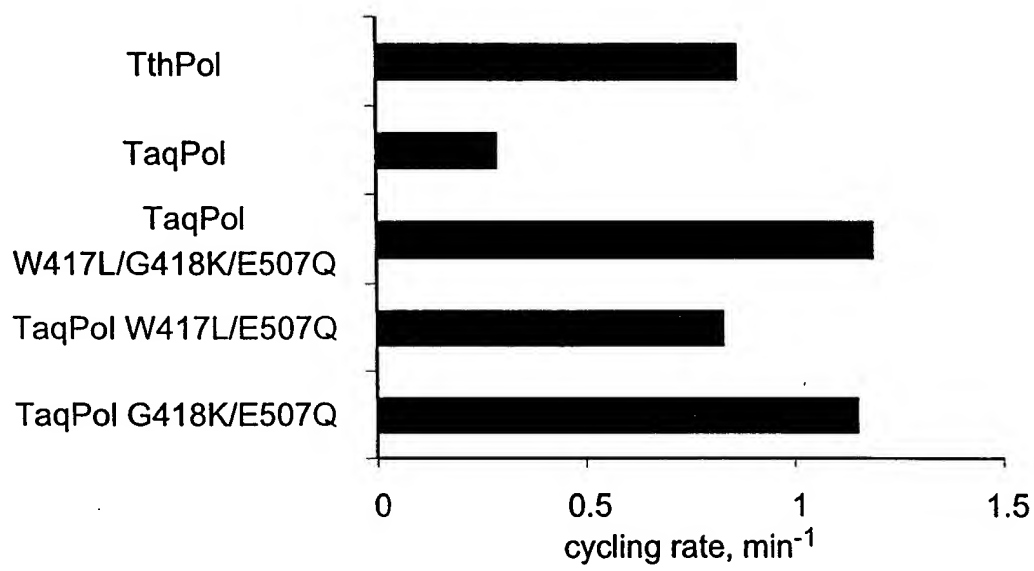


FIGURE 15


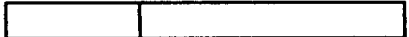




		Polymerase Activity Assays	
		<u>% Fl-labeled dUTP incorporated</u>	
		<u>RNA, p(A) or DNA, p(dA) Template</u>	
	Nuclease Domain Polymerase Domain		
Tth		5.8 (1.00)	14.8 (1.00)
Taq		0.8 (0.14)	15.0 (1.01)
TaqTth(N)		4.88 (0.84)	12.9 (0.87)
TaqTth(N-B)		0.58 (0.10)	13.3 (0.90)
TaqTth(B-S)		6.60 (1.14)	14.9 (1.01)
Taq(W417L/G418K/E507Q)		0.42 (0.07)	12.6 (0.85)

FIGURE 16

004230-402250



FIGURE 17

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

FIGURE 18A

004250" 40642500

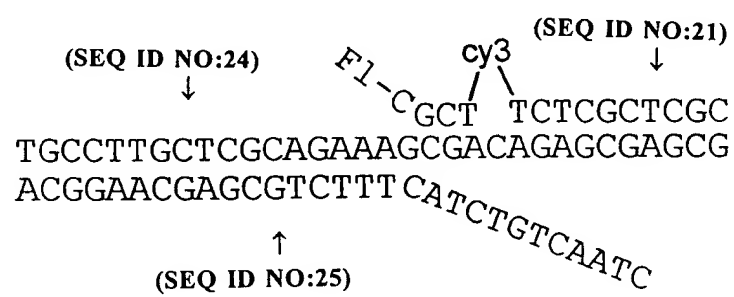


FIGURE 18C

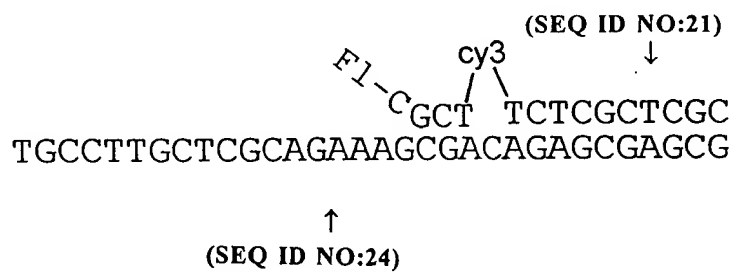


FIGURE 18D

09577204.024400

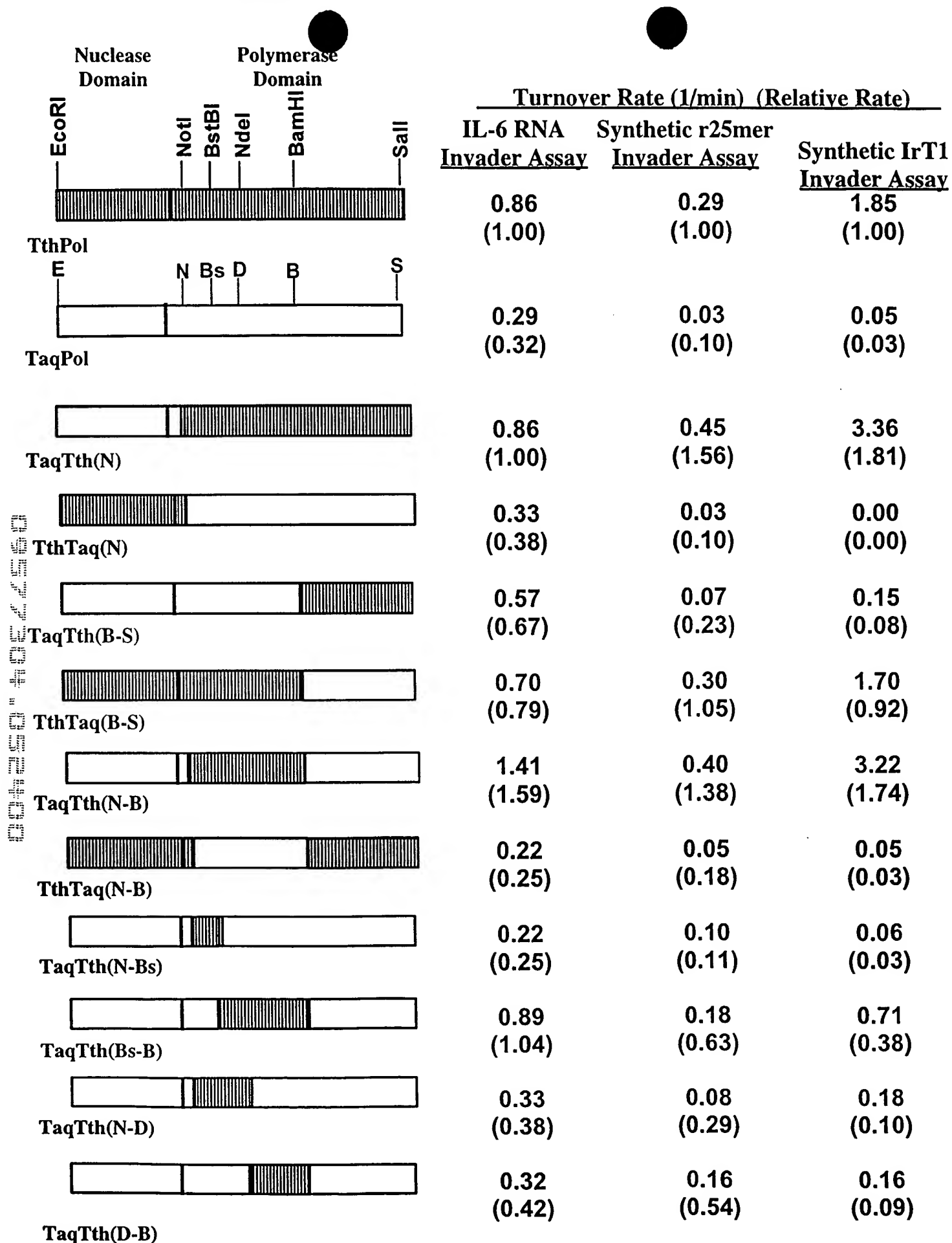


FIGURE 19

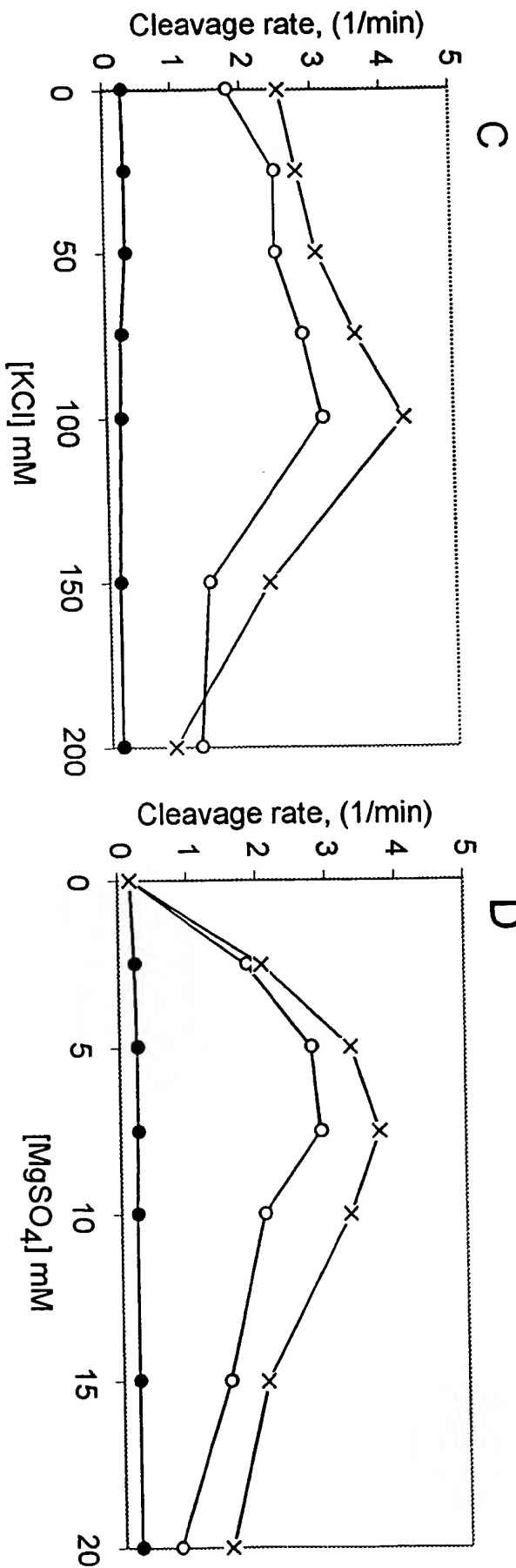
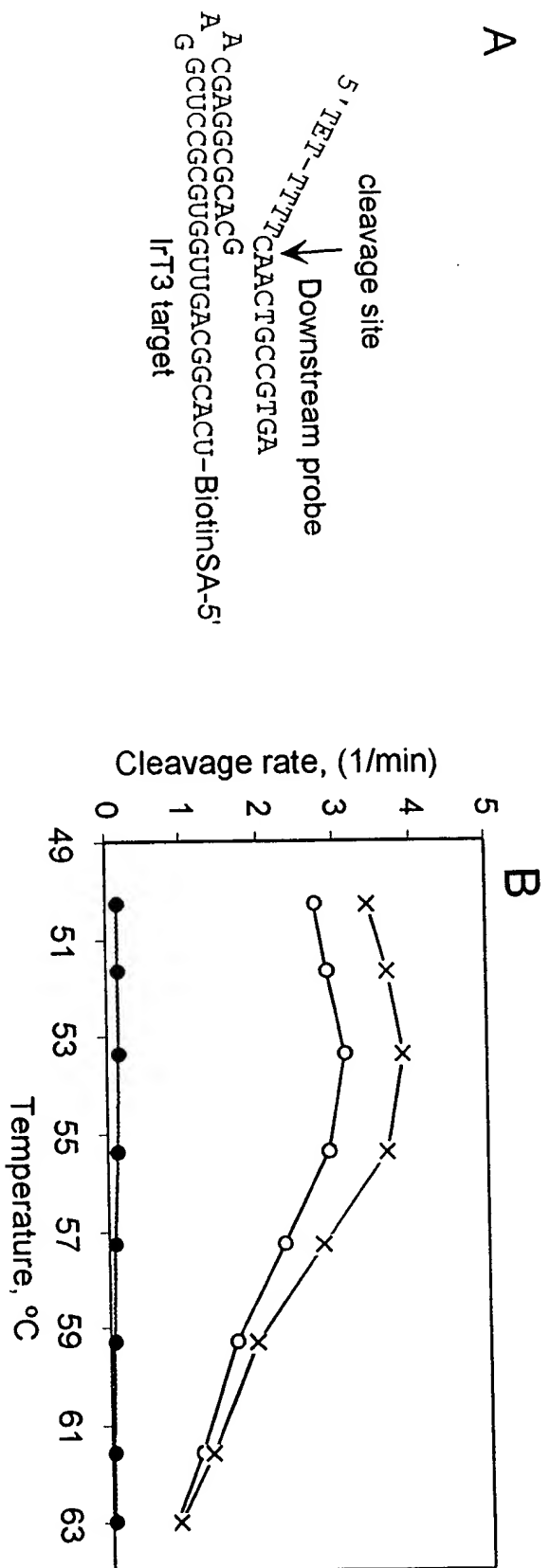


FIGURE 20

09577304.052400

[illegible]

5'-tet-TTTTCAACTGCCGTGA
A CGAGGCGCACG
A GCTCCGCGTGGTTGACGGCACT

5'-tet-TTTTCAACTGCCGTGA
A CGAGGCGCACG
A GCUCCGCGUGGUUGACGGCACU-BiotinSA-5'

FIGURE 22

A

(SEQ ID NO:29)



3' NH4-AATTGCTCCGCGTGGTTGACGAAGGAGGC-5'

5'-F1-TCCTTCTCAACTGCTTCCTCCG-3'



(SEQ ID NO:30)

B

(SEQ ID NO:31)



5'-AACGAGGCGCACCTCAAATCTCCCTTT-biotin

(SEQ ID NO:29)



3' NH4-AATTGCTCCGCGTGGTTGACGAAGGAGGC-5'

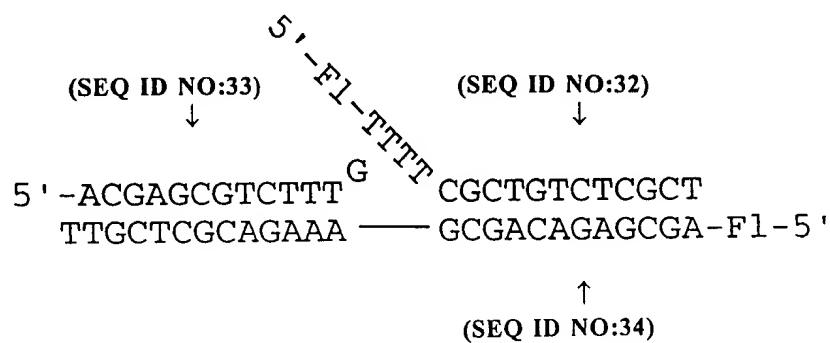
5'-F1-TCCTTCTCAACTGCTTCCTCCG-3'



(SEQ ID NO:30)

004230-40324000

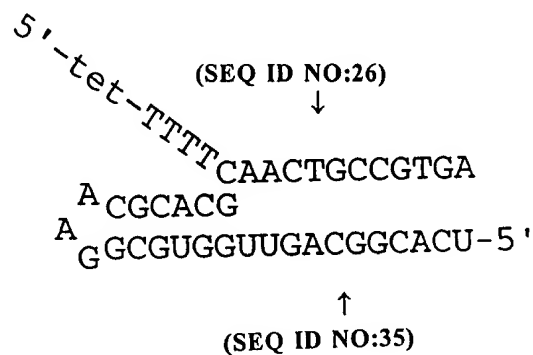
FIGURE 23



004250"404250"

FIGURE 24

A



B



004230 402430

FIGURE 25

